

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Hiroyuki NAKANE, Chikara OHTO, Shinichi OHNUMA, Kazutake HIROOKA, Tokuzo NISHINO

(ii) TITLE OF INVENTION: Farnesyl Diphosphate Synthase

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Kenyon & Kenyon
- (B) STREET: One Broadway
- (C) CITY: New York
- (D) STATE: NY
- (E) COUNTRY: USA
- (F) ZIP: 10004

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3½ Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
- (D) SOFTWARE: WordPerfect 6.1 Windows

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Not Yet Issued
- (B) FILING DATE: Concurrent Herewith
- (C) CLASSIFICATION: Not Yet Issued

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: JP 8-213211
- (B) FILING DATE: 24-JUL-96

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Edward W. Greason
- (B) REGISTRATION NUMBER: 18,918
- (C) REFERENCE/DOCKET NUMBER: 77670/495

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212)425-7200
- (B) TELEFAX: (212)425-5288

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sulfolobus acidocaldarius*  
(B) STRAIN: ATCC 33909

(ix) FEATURE:

(A) KEY: Asp-rich domain  
(B) LOCATION: 82-86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ser Tyr Phe Asp Asn Tyr Phe Asn Glu Ile Val Asn Ser Val Asn  
5 10 15  
Asp Ile Ile Lys Ser Tyr Ile Ser Gly Asp Val Pro Lys Leu Tyr Glu  
20 25 30  
Ala Ser Tyr His Leu Phe Thr Ser Gly Gly Lys Arg Leu Arg Pro Leu  
35 40 45  
Ile Leu Thr Ile Ser Ser Asp Leu Phe Gly Gly Gln Arg Glu Arg Ala  
50 55 60  
Tyr Tyr Ala Gly Ala Ala Ile Glu Val Leu His Thr Phe Thr Leu Val  
65 70 75 80  
His Asp Asp Ile Met Asp Gln Asp Asn Ile Arg Arg Gly Leu Pro Thr  
85 90 95  
Val His Val Lys Tyr Gly Leu Pro Leu Ala Ile Leu Ala Gly Asp Leu  
100 105 110  
Leu His Ala Lys Ala Phe Gln Leu Leu Thr Gln Ala Leu Arg Gly Leu  
115 120 125  
Pro Ser Glu Thr Ile Ile Lys Ala Phe Asp Ile Phe Thr Arg Ser Ile  
130 135 140  
Ile Ile Ile Ser Glu Gly Gln Ala Val Asp Met Glu Phe Glu Asp Arg  
145 150 155 160  
Ile Asp Ile Lys Glu Gln Glu Tyr Leu Asp Met Ile Ser Arg Lys Thr  
165 170 175  
Ala Ala Leu Phe Ser Ala Ser Ser Ser Ile Gly Ala Leu Ile Ala Gly  
180 185 190  
Ala Asn Asp Asn Asp Val Arg Leu Met Ser Asp Phe Gly Thr Asn Leu  
195 200 205  
Gly Ile Ala Phe Gln Ile Val Asp Asp Ile Leu Gly Leu Thr Ala Asp  
210 215 220  
Glu Lys Glu Leu Gly Lys Pro Val Phe Ser Asp Ile Arg Glu Gly Lys  
225 230 235 240  
Lys Thr Ile Leu Val Ile Lys Thr Leu Glu Leu Cys Lys Glu Asp Glu

				245					250					255					
Lys	Lys	Ile	Val	Leu	Lys	Ala	Leu	Gly	Asn	Lys	Ser	Ala	Ser	Lys	Glu				
			260					265					270						
Glu	Leu	Met	Ser	Ser	Ala	Asp	Ile	Ile	Lys	Lys	Tyr	Ser	Leu	Asp	Tyr				
		275					280					285							
Ala	Tyr	Asn	Leu	Ala	Glu	Lys	Tyr	Tyr	Lys	Asn	Ala	Ile	Asp	Ser	Leu				
	290					295					300								
Asn	Gln	Val	Ser	Ser	Lys	Ser	Asp	Ile	Pro	Gly	Lys	Ala	Leu	Lys	Tyr				
305					310					315					320				
Leu	Ala	Glu	Phe	Thr	Ile	Arg	Arg	Arg	Lys										
				325					330										

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sulfolobus acidocaldarius*
- (B) STRAIN: ATCC 33909

(ix) FEATURE:

- (A) KEY: Asp-rich domain coding
- (B) LOCATION: 246-258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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ATGAGTTACT TTGACAACTA TTTTAATGAG ATTGTTAATT CTGTAAACGA CATTATTAAG   60
AGCTATATAT CTGGAGATGT TCCTAAACTA TATGAAGCCT CATATCATTT GTTTACATCT   120
GGAGGTAAGA GGTAAAGACC ATTAATCTTA ACTATATCAT CAGATTTATT CGGAGGACAG   180
AGAGAAAGAG CTTATTATGC AGGTGCAGCT ATTGAAGTTC TTCATACTTT TACGCTTGTG   240
CATGATGATA TTATGGATCA AGATAATATC AGAAGAGGGT TACCCACAGT CCACGTGAAA   300
TACGGCTTAC CCTTAGCAAT ATTAGCTGGG GATTTACTAC ATGCAAAGGC TTTTCAGCTC   360
TTAACCCAGG CTCTTAGAGG TTTGCCAAGT GAAACCATAA TTAAGGCTTT CGATATTTTC   420
ACTCGTTCAA TAATAATTAT ATCCGAAGGA CAGGCAGTAG ATATGGAATT TGAGGACAGA   480

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ATTGATATAA AGGAGCAGGA ATACCTTGAC ATGATCTCAC GTAAGACAGC TGCATTATTC 540  
TCGGCATCCT CAAGTATAGG CGCACTTATT GCTGGTGCTA ATGATAATGA TGTAAGACTG 600  
ATGTCTGATT TCGGTACGAA TCTAGGTATT GCATTTTCTAGA TTGTTGACGA TATCTTAGGT 660  
CTAACAGCAG ACGAAAAGGA ACTTGGAAG CCTGTTTTTA GTGATATTAG GGAGGGTAAA 720  
AAGACTATAC TTGTAATAAA AACACTGGAG CTTTGTAAG AGGACGAGAA GAAGATTGTC 780  
CTAAAGGCGT TAGGTAATAA GTCAGCCTCA AAAGAAGAAT TAATGAGCTC AGCAGATATA 840  
ATTAAGAAAT ACTCTTTAGA TTATGCATAC AATTTAGCAG AGAAATATTA TAAAAATGCT 900  
ATAGACTCTT TAAATCAAGT CTCCTCTAAG AGTGATATAC CTGGAAAGGC TTAAAAATAT 960  
CTAGCTGAAT TTACGATAAG AAGGAGAAAA TAA 993

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATACTTTTT TCCTTGTGGC TGATGATATC ATGGATC

37

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATACTTTTT TCCTTGTGCT TGATGATATC ATGGATC

37

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATACTTATT TCCTTGTGCT TGATGATATC ATGGATC

37

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATACTTATT TCCTTGTGGC TGATGATATC ATGGATC

37

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTCTTCATA CTTATTCGCT TATTCATGAT AGTATT

36

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTCATGATG ATCTTCCATC GATGGATCAA GAT

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTTCCTTG TGGCTGATGA TATCATG

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTTCCTTG TGCTTGATGA TATCATG

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATTCCTTG TGCTTGATGA TATCATG

27

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TATTCCTTG TGGCTGATGA TATCATG

27

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TATTCGCTTA TTCATGATGA TCTTCCATCG ATG

33

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

32

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTACGCTTG TGCATGATGA TATTATG

27

00095560.072297  
252220.09586880